GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 21, 2004, 08:45:56 ; Search time 23.5 Seconds
(without alignments)
8919.210 Million cell updates/sec

Title: US-09-602-362E-15
Perfect score: 3403
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=721.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=35
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3261	95.8	1002	4	US-09-620-405B-475	Sequence 475, App
2	3261	95.8	1002	4	US-09-604-287A-475	Sequence 475, App
3	3261	95.8	1002	4	US-09-834-759-475	Sequence 475, App
4	3261	95.8	1095	4	US-09-620-405B-493	Sequence 493, App
5	3261	95.8	1095	4	US-09-834-759-493	Sequence 493, App
6	2184	64.2	445	4	US-09-620-405B-473	Sequence 473, App
7	2184	64.2	445	4	US-09-433-826B-473	Sequence 473, App
8	2184	64.2	445	4	US-09-604-287A-473	Sequence 473, App
9	2184	64.2	445	4	US-09-834-759-473	Sequence 473, App
10	2017	59.3	432	4	US-09-389-681-181	Sequence 181, App
11	2017	59.3	432	4	US-09-620-405B-181	Sequence 181, App
12	2017	59.3	432	4	US-09-339-338-181	Sequence 181, App
13	2017	59.3	432	4	US-09-433-826B-181	Sequence 181, App
14	2017	59.3	432	4	US-09-604-287A-181	Sequence 181, App
15	2017	59.3	432	4	US-09-285-480-181	Sequence 181, App
16	2017	59.3	432	4	US-09-834-759-181	Sequence 181, App
17	1597.5	46.9	650	4	US-09-620-405B-469	Sequence 469, App
18	1597.5	46.9	650	4	US-09-433-826B-469	Sequence 469, App
19	1597.5	46.9	650	4	US-09-604-287A-469	Sequence 469, App
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21	1597.5	46.9	743	4	US-09-620-405B-494	Sequence 494, App
22	1597.5	46.9	743	4	US-09-834-759-494	Sequence 494, App
23	1404.5	41.3	410	4	US-09-620-405B-495	Sequence 495, App
24	1404.5	41.3	410	4	US-09-834-759-495	Sequence 495, App
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26	1397	41.1	317	4	US-09-620-405B-176	Sequence 176, App
27	1397	41.1	317	4	US-09-339-338-176	Sequence 176, App
28	1397	41.1	317	4	US-09-433-826B-176	Sequence 176, App
29	1397	41.1	317	4	US-09-604-287A-176	Sequence 176, App
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32	1397	41.1	323	4	US-09-620-405B-483	Sequence 483, App
33	1397	41.1	323	4	US-09-604-287A-483	Sequence 483, App
34	1397	41.1	323	4	US-09-834-759-483	Sequence 483, App
35	1070.5	31.5	466	4	US-09-620-405B-472	Sequence 472, App
36	1070.5	31.5	466	4	US-09-433-826B-472	Sequence 472, App
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39	847.5	24.9	179	4	US-09-389-681-179	Sequence 179, App
40	847.5	24.9	179	4	US-09-620-405B-179	Sequence 179, App
41	847.5	24.9	179	4	US-09-339-338-179	Sequence 179, App
42	847.5	24.9	179	4	US-09-433-826B-179	Sequence 179, App
43	847.5	24.9	179	4	US-09-604-287A-179	Sequence 179, App
44	847.5	24.9	179	4	US-09-285-480-179	Sequence 179, App
45	847.5	24.9	179	4	US-09-834-759-179	Sequence 179, App

ALIGNMENTS

RESULT 1
US-09-620-405B-475
; Sequence 475, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 475
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1002)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-620-405B-475

Alignment Scores:

Pred. No.:	2.51e-300	Length:	1002
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Percent Similarity:	97.19%	Conservative:	3
Best Local Similarity:	96.75%	Mismatches:	15
Query Match:	95.83%	Indels:	5
DB:	4	Gaps:	0

US-09-602-362E-15 (1-2030) x US-09-620-405B-475 (1-1002)

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Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
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Db        906 etTyrGlnAsnGluGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspG 926

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Db        946 is-LysLysAlaAspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLys 965

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Qy       1988 AAAAACCCGTATATTTCAATATGGAAAAAAAAAAANAAAAA 2027
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Db        986 LysAsn-ArgIleTyrGlnTyrGluLysGluLysAlaGlu 998
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RESULT 2
US-09-604-287A-475
; Sequence 475, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

```
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C7
;  CURRENT APPLICATION NUMBER: US/09/604,287A
;  CURRENT FILING DATE:  2000-06-22
;  NUMBER OF SEQ ID NOS: 489
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 475
;   LENGTH: 1002
;   TYPE: PRT
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1002)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-604-287A-475

Alignment Scores:
Pred. No.:              2.51e-300      Length:          1002
Score:                  3261.00        Matches:         654
Percent Similarity:     97.19%         Conservative:    3
Best Local Similarity:  96.75%         Mismatches:      15
Query Match:            95.83%         Indels:          5
DB:                     4              Gaps:            0

US-09-602-362E-15 (1-2030) x US-09-604-287A-475 (1-1002)

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Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
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Db        347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 366

Qy        129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
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Qy        189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 406

Qy        249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
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Db        407 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 426

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Db        427 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 446

Qy        369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
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Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
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Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
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Db        507 ThrLeuArgAlaAspGlnMetProSerGluSerLysGlnLys***ValGluGluAsn 526

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Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
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Db        547 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 566

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
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Db        567 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 586

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 606

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 626

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAla 646

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 AspIleLeuAsnGluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLys 666

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 GluLeuGluValLysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLys 686

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 SerValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeu 706

Qy       1149 CATGAAAATTGCATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTG 1208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 HisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeu 726

Qy       1209 AAACACCAATACCAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAA 1268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 LysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGlu 746

Qy       1269 AAGAATGCTGAACTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCA 1328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 LysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAla 766

Qy       1329 TCTCAATATAGTGGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAA 1388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 SerGlnTyrSerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLys 786

Qy       1389 TTGAAGGAAAAACAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGA 1448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 LeuLysGluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArg 806

Qy       1449 CTGGCTTCTGCTGTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCT 1508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 LeuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluPro 826

Qy       1509 GCTTTCCACATTGCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGT 1568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSer 846

Qy       1569 ACCGATATATAACAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCAN 1628
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 Thr-IleTyrAsnAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLy 866

Qy       1629 AAGCCTAAAAATTAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTC 1688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        866 sSerLeuLysIleAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSe 886

Qy       1689 AGGAACATGCACAAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACA 1748
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 r-GluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisM 906
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Qy       1749 TGTNTCAAANCGAACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATC 1808
Db        906 etTyrGlnAsnGluGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspG 926

Qy       1809 AGAAATTATTTCAACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCAC 1868
Db        926 lnLysLeuPheGlnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaH 946

Qy       1869 ATAANGAAAGCTGACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAA 1928
Db        946 is-LysLysAlaAspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLys 965

Qy       1929 ATGCN-CATCATCTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCATTTA 1987
Db        966 MetGlnHisHisLeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeu 985

Qy       1988 AAAAACCCGTATATTTCAATATGGAAAAAAAAAANAAAAA 2027
Db        986 LysAsn-ArgIleTyrGlnTyrGluLysGluLysAlaGlu 998

RESULT 3
US-09-834-759-475
; Sequence 475, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C9
;  CURRENT APPLICATION NUMBER: US/09/834,759
;  CURRENT FILING DATE:  2001-04-13
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 475
;   LENGTH: 1002
;   TYPE: PRT
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1002)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-834-759-475

Alignment Scores:
Pred. No.:              2.51e-300       Length:         1002
Score:                  3261.00         Matches:        654
Percent Similarity:     97.19%          Conservative:   3
Best Local Similarity:  96.75%          Mismatches:     15
Query Match:            95.83%          Indels:         5
DB:                     4               Gaps:           0

US-09-602-362E-15 (1-2030) x US-09-834-759-475 (1-1002)

Qy          9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
Db        327 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 346

Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
Db        347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 366

Qy        129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
Db        367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 386

Qy        189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
Db        387 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 406

Qy        249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
Db        407 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 426

Qy        309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
Db        427 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 446

Qy        369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
Db        447 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 466

Qy        429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
Db        467 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 486

Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
Db        487 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 506

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
Db        507 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 526

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
Db        527 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 546

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
Db        547 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 566

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
Db        567 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 586

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
Db        587 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 606

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
Db        607 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 626

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
Db        627 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAla 646

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028
Db        647 AspIleLeuAsnGluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLys 666

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088
Db        667 GluLeuGluValLysGlnGlnLeuGluLeuGluAlaLeuArgIleGlnAspIleGluLeuLys 686

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
Db        687 SerValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeu 706

Qy       1149 CATGAAAATTGCATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTG 1208
Db        707 HisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeu 726

Qy       1209 AAACACCAATACCAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAA 1268
Db        727 LysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGlu 746

Qy       1269 AAGAATGCTGAACTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCA 1328
Db        747 LysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAla 766
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Qy       1329 TCTCAATATAGTGGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAA 1388
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 SerGlnTyrSerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLys 786

Qy       1389 TTGAAGGAAAAACAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGA 1448
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 LeuLysGluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArg 806

Qy       1449 CTGGCTTCTGCTGTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCT 1508
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 LeuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluPro 826

Qy       1509 GCTTTCCACATTGCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGT 1568
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSer 846

Qy       1569 ACCGATATATAACAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCAN 1628
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 Thr-IleTyrAsnAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLy 866

Qy       1629 AAGCCTAAAAATTAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTC 1688
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        866 sSerLeuLysIleAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSe 886

Qy       1689 AGGAACATGCACAAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACA 1748
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 r-GluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisM 906

Qy       1749 TGTNTCAAANCGAACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATC 1808
             ||   |||   |||||||||   ||||||||||||||||   ||||||||||||||||||||
Db        906 etTyrGlnAsnGluGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspG 926

Qy       1809 AGAAATTATTTCAACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCAC 1868
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        926 lnLysLeuPheGlnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaH 946

Qy       1869 ATAANGAAAGCTGACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAA 1928
             ||   ||||||||||||||||||||||||||||||||   |||   ||||||||||||||
Db        946 is-LysLysAlaAspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLys 965

Qy       1929 ATGCN-CATCATCTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCATTTA 1987
             |||   |||||||||||||||||||||||||||||||||   |||   |||||||||
Db        966 MetGlnHisHisLeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeu 985

Qy       1988 AAAAACCCGTATATTTCAATATGGAAAAAAAAAANAAAAA 2027
             |||||| ||||||:::|||||||   |||:::|||   :::
Db        986 LysAsn-ArgIleTyrGlnTyrGluLysGluLysAlaGlu 998
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RESULT 4
US-09-620-405B-493
; Sequence 493, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 493
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(1095)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-620-405B-493

Alignment Scores:

Pred. No.:	2.59e-300	Length:	1095
Score:	3261.00	Matches:	654
Percent Similarity:	97.19%	Conservative:	3
Best Local Similarity:	96.75%	Mismatches:	15
Query Match:	95.83%	Indels:	5
DB:	4	Gaps:	0

US-09-602-362E-15 (1-2030) x US-09-620-405B-493 (1-1095)

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Qy          9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 439

Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 459

Qy        129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 479

Qy        189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 499

Qy        249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 519

Qy        309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 539

Qy        369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 559

Qy        429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 579

Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 599

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
              ||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        600 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 619

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 639

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 659

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 679

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 699

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 719
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Qy       909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
Db       720 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAla 739

Qy       969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028
Db       740 AspIleLeuAsnGluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLys 759

Qy      1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088
Db       760 GluLeuGluValLysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLys 779

Qy      1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
Db       780 SerValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeu 799

Qy      1149 CATGAAAATTGCATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTG 1208
Db       800 HisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeu 819

Qy      1209 AAACACCAATACCAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAA 1268
Db       820 LysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGlu 839

Qy      1269 AAGAATGCTGAACTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCA 1328
Db       840 LysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAla 859

Qy      1329 TCTCAATATAGTGGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAA 1388
Db       860 SerGlnTyrSerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLys 879

Qy      1389 TTGAAGGAAAAACAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGA 1448
Db       880 LeuLysGluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArg 899

Qy      1449 CTGGCTTCTGCTGTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCT 1508
Db       900 LeuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluPro 919

Qy      1509 GCTTTCCACATTGCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGT 1568
Db       920 AlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSer 939

Qy      1569 ACCGATATATAACAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCAN 1628
Db       940 Thr-IleTyrAsnAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLy 959

Qy      1629 AAGCCTAAAAATTAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTC 1688
Db       959 sSerLeuLysIleAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSe 979

Qy      1689 AGGAACATGCACAAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACA 1748
Db       979 r-GluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisM 999

Qy      1749 TGTNTCAAANCGAACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATC 1808
Db       999 etTyrGlnAsnGluGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspG 1019

Qy      1809 AGAAATTATTTCAACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCAC 1868
Db       1019 lnLysLeuPheGlnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaH 1039

Qy      1869 ATAANGAAAGCTGACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAA 1928
Db       1039 is-LysLysAlaAspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLys 1058

Qy      1929 ATGCN-CATCATCTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCATTTA 1987
Db       1059 MetGlnHisHisLeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeu 1078

Qy      1988 AAAAACCCGTATATTTCAATATGGAAAAAAAAAANAAAAA 2027
Db       1079 LysAsn-ArgIleTyrGlnTyrGluLysGluLysAlaGlu 1091
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RESULT 5
US-09-834-759-493
; Sequence 493, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 493
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(1095)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-834-759-493

Alignment Scores:

Pred. No.:	2.59e-300	Length:	1095
Score:	3261.00	Matches:	654
Percent Similarity:	97.19%	Conservative:	3
Best Local Similarity:	96.75%	Mismatches:	15
Query Match:	95.83%	Indels:	5
DB:	4	Gaps:	0

US-09-602-362E-15 (1-2030) x US-09-834-759-493 (1-1095)

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Qy         9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
Db       420 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 439

Qy        69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
Db       440 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 459

Qy       129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
Db       460 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 479

Qy       189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
Db       480 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 499

Qy       249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
Db       500 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 519

Qy       309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
Db       520 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 539

Qy       369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
Db       540 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 559

Qy       429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
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Db        560 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 579

Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 599

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 619

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 639

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 659

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 679

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 699

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 719

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAla 739

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 AspIleLeuAsnGluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLys 759

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 GluLeuGluValLysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLys 779

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 SerValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeu 799

Qy       1149 CATGAAAATTGCATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTG 1208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 HisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeu 819

Qy       1209 AAACACCAATACCAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAA 1268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 LysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGlu 839

Qy       1269 AAGAATGCTGAACTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCA 1328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 LysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAla 859

Qy       1329 TCTCAATATAGTGGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAA 1388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 SerGlnTyrSerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLys 879

Qy       1389 TTGAAGGAAAAACAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGA 1448
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Db        880 LeuLysGluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArg 899

Qy       1449 CTGGCTTCTGCTGTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCT 1508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 LeuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluPro 919

Qy       1509 GCTTTCCACATTGCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGT 1568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 AlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSer 939

Qy       1569 ACCGATATATAACAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCAN 1628
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 Thr-IleTyrAsnAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLy 959

Qy       1629 AAGCCTAAAAATTAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTC 1688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 sSerLeuLysIleAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSe 979

Qy       1689 AGGAACATGCACAAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACA 1748
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 r-GluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisM 999

Qy       1749 TGTNTCAAANCGAACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATC 1808
              ||   |||   |||||||||   ||||||||||||||   ||||||||||||||||||
Db        999 etTyrGlnAsnGluGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspG 1019

Qy       1809 AGAAATTATTTCAACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCAC 1868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 lnLysLeuPheGlnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaH 1039

Qy       1869 ATAANGAAAGCTGACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAA 1928
              ||   ||||||||||||||||||||||||||||||   |||   ||||||||||||
Db       1039 is-LysLysAlaAspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLys 1058

Qy       1929 ATGCN-CATCATCTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCATTTA 1987
              |||   ||||||||||||||||||||||||||||||   |||   |||||||||
Db       1059 MetGlnHisHisLeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeu 1078

Qy       1988 AAAAACCCGTATATTTCAATATGGAAAAAAAAAAANAAAAA 2027
              |||||| ||||||:::||||||   |||:::|||   :::
Db       1079 LysAsn-ArgIleTyrGlnTyrGluLysGluLysAlaGlu 1091
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RESULT 6
US-09-620-405B-473
; Sequence 473, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 473
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-405B-473

Alignment Scores:

Pred. No.:	1.82e-198	Length:	445
Score:	2184.00	Matches:	427
Percent Similarity:	99.77%	Conservative:	0
Best Local Similarity:	99.77%	Mismatches:	1
Query Match:	64.18%	Indels:	0
DB:	4	Gaps:	0

US-09-602-362E-15 (1-2030) x US-09-620-405B-473 (1-445)

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Qy          9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
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Db         15 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 34

Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        35 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 54

Qy       129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        55 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 74

Qy       189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        75 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 94

Qy       249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        95 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 114

Qy       309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
             ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       115 LysAlaAlaHisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 134

Qy       369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       135 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 154

Qy       429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       155 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 174

Qy       489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       175 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 194

Qy       549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       195 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLysLysValGluGluAsn 214

Qy       609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       215 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 234

Qy       669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       235 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 254

Qy       729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       255 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 274

Qy       789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       275 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 294

Qy       849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       295 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 314

Qy       909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       315 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAla 334

Qy       969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       335 AspIleLeuAsnGluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLys 354

Qy      1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       355 GluLeuGluValLysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLys 374

Qy      1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       375 SerValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeu 394

Qy      1149 CATGAAAATTGCATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTG 1208
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Db       395 HisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeu 414

Qy      1209 AAACACCAATACCAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAA 1268
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Db       415 LysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGlu 434

Qy      1269 AAGAATGCTGAACTTCAGATGACC 1292
             ||||||||||||||||||||||||
Db       435 LysAsnAlaGluLeuGlnMetThr 442
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RESULT 7
US-09-433-826B-473
; Sequence 473, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 473
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-433-826B-473

Alignment Scores:

Pred. No.:	1.82e-198	Length:	445
Score:	2184.00	Matches:	427
Percent Similarity:	99.77%	Conservative:	0
Best Local Similarity:	99.77%	Mismatches:	1
Query Match:	64.18%	Indels:	0
DB:	4	Gaps:	0

US-09-602-362E-15 (1-2030) x US-09-433-826B-473 (1-445)

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Qy         9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
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Db        15 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 34

Qy        69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        35 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 54

Qy       129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        55 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 74

Qy       189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        75 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 94

Qy       249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        95 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 114

Qy       309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
             ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       115 LysAlaAlaHisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 134

Qy       369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       135 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 154

Qy       429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       155 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 174
```

```
Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 194

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLysLysValGluGluAsn 214

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 234

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 254

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 274

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 294

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 314

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAla 334

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 AspIleLeuAsnGluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLys 354

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 GluLeuGluValLysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLys 374

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 SerValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeu 394

Qy       1149 CATGAAAATTGCATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTG 1208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 HisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeu 414

Qy       1209 AAACACCAATACCAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAA 1268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 LysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGlu 434

Qy       1269 AAGAATGCTGAACTTCAGATGACC 1292
              ||||||||||||||||||||||||
Db        435 LysAsnAlaGluLeuGlnMetThr 442
```

RESULT 8
US-09-604-287A-473
; Sequence 473, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 473
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-287A-473

Alignment Scores:

Pred. No.:	1.82e-198	Length:	445
Score:	2184.00	Matches:	427
Percent Similarity:	99.77%	Conservative:	0
Best Local Similarity:	99.77%	Mismatches:	1
Query Match:	64.18%	Indels:	0
DB:	4	Gaps:	0

US-09-602-362E-15 (1-2030) x US-09-604-287A-473 (1-445)

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Qy          9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         15 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 34

Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 54

Qy        129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 74

Qy        189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 94

Qy        249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 114

Qy        309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 LysAlaAlaHisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 134

Qy        369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 154

Qy        429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 174

Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 194

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLysLysValGluGluAsn 214

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 234

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 254

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 274

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 294
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Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
Db        295 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 314

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
Db        315 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAla 334

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028
Db        335 AspIleLeuAsnGluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLys 354

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088
Db        355 GluLeuGluValLysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLys 374

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
Db        375 SerValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeu 394

Qy       1149 CATGAAAATTGCATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTG 1208
Db        395 HisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeu 414

Qy       1209 AAACACCAATACCAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAA 1268
Db        415 LysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGlu 434

Qy       1269 AAGAATGCTGAACTTCAGATGACC 1292
Db        435 LysAsnAlaGluLeuGlnMetThr 442

RESULT 9
US-09-834-759-473
; Sequence 473, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C9
;  CURRENT APPLICATION NUMBER: US/09/834,759
;  CURRENT FILING DATE:  2001-04-13
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 473
;   LENGTH: 445
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-759-473

Alignment Scores:
Pred. No.:                1.82e-198      Length:          445
Score:                    2184.00        Matches:         427
Percent Similarity:       99.77%         Conservative:    0
Best Local Similarity:    99.77%         Mismatches:      1
Query Match:              64.18%         Indels:          0
DB:                       4              Gaps:            0

US-09-602-362E-15 (1-2030) x US-09-834-759-473 (1-445)

Qy          9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
Db         15 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 34

Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
Db         35 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 54

Qy        129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
Db         55 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 74

Qy        189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
Db         75 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 94

Qy        249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
Db         95 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 114

Qy        309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
Db        115 LysAlaAlaHisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 134

Qy        369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
Db        135 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 154

Qy        429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
Db        155 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 174

Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
Db        175 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 194

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
Db        195 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLysLysValGluGluAsn 214

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
Db        215 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 234

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
Db        235 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 254

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
Db        255 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 274

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
Db        275 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 294

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
Db        295 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 314

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
Db        315 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAla 334

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028
Db        335 AspIleLeuAsnGluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLys 354

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088
Db        355 GluLeuGluValLysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLys 374

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
Db        375 SerValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeu 394

Qy       1149 CATGAAAATTGCATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTG 1208
```

```
Db        395 HisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeu 414

Qy       1209 AAACACCAATACCAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAA 1268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 LysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGlu 434

Qy       1269 AAGAATGCTGAACTTCAGATGACC 1292
              |||||||||||||||||||||||||
Db        435 LysAsnAlaGluLeuGlnMetThr 442

RESULT 10
US-09-389-681-181
; Sequence 181, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
;  APPLICANT: Yuqui, Jiang
;  APPLICANT: Dillon, Davin C.
;  APPLICANT: Mitcham, Jennifer L.
;  APPLICANT: Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
;  TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.470C3
;  CURRENT APPLICATION NUMBER: US/09/389,681A
;  CURRENT FILING DATE: 1999-09-02
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 181
;   LENGTH: 432
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-389-681-181

Alignment Scores:
Pred. No.:                1.17e-182      Length:          432
Score:                    2017.00        Matches:         412
Percent Similarity:       96.06%         Conservative:    3
Best Local Similarity:    95.37%         Mismatches:      13
Query Match:              59.27%         Indels:          5
DB:                       4              Gaps:            0

US-09-602-362E-15 (1-2030) x US-09-389-681-181 (1-432)

Qy        741 GATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCACTGTGAACAACGT 800
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Db          1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20

Qy        801 ACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAGAAACTGTCAGAA 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGlu 40

Qy        861 GCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGC 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 AlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCys 60

Qy        921 AGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCCGATATATTAAAT 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SerValArgLeuThrLeuAsnGlnGluGluLysArgArgAsnAlaAspIleLeuAsn 80

Qy        981 GAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAAGAGTTAGAAGTG 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 GluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluVal 100

Qy       1041 AAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAGAGTGTAGAAAGT 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSer 120

Qy       1101 AATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGC 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140

Qy       1161 ATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATAC 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 MetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyr 160

Qy       1221 CAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAA 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGlu 180

Qy       1281 CTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGT 1340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSer 200

Qy       1341 GGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAA 1400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220

Qy       1401 CAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCT 1460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 GlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAla 240

Qy       1461 GTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATT 1520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIle 260

Qy       1521 GCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAA 1580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAs 280

Qy       1581 CAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAAT 1640
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        280 nAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIl 300

Qy       1641 TAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCAC 1700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaG 320

Qy       1701 AAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCG 1760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||  |
Db        320 lnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340

Qy       1761 AACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTC 1820
              ||||||||  ||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        340 luGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheG 360

Qy       1821 AACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCT 1880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        360 lnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAla 379

Qy       1881 GACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCAT 1939
              ||||||||||||||||||||||||||  |||  |||||||||||||||  |||||||
Db        380 AspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHis 399

Qy       1940 CTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTAT 1999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 LeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIl 419

Qy       2000 ATTTCAATATGGAAAAAAAAAAANAAAAA 2027
              |:::|||||  |||:::|||  :::
Db        419 eTyrGlnTyrGluLysGluLysAlaGlu 428

RESULT 11
US-09-620-405B-181
; Sequence 181, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C8
;  CURRENT APPLICATION NUMBER: US/09/620,405B
;  CURRENT FILING DATE:  2000-07-20
```

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;  NUMBER OF SEQ ID NOS: 495
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 181
;   LENGTH: 432
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-620-405B-181

Alignment Scores:
Pred. No.:              1.17e-182       Length:         432
Score:                  2017.00         Matches:        412
Percent Similarity:     96.06%          Conservative:   3
Best Local Similarity:  95.37%          Mismatches:     13
Query Match:            59.27%          Indels:         5
DB:                     4               Gaps:           0

US-09-602-362E-15 (1-2030) x US-09-620-405B-181 (1-432)

Qy        741 GATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCACTGTGAACAACGT 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20

Qy        801 ACAGGAAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAGAAACTGTCAGAA 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGlu 40

Qy        861 GCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGC 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 AlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCys 60

Qy        921 AGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCCGATATATTTAAAT 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAlaAspIleLeuAsn 80

Qy        981 GAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAAGAGTTAGAAGTG 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 GluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluVal 100

Qy       1041 AAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAGAGTGTAGAAAGT 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSer 120

Qy       1101 AATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGC 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140

Qy       1161 ATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATAC 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 MetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyr 160

Qy       1221 CAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAA 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGlu 180

Qy       1281 CTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGT 1340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSer 200

Qy       1341 GGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAA 1400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220

Qy       1401 CAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCT 1460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 GlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAla 240

Qy       1461 GTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATT 1520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIle 260

Qy       1521 GCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAA 1580
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAs 280

Qy       1581 CAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAAT 1640
              |||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db        280 nAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIl 300

Qy       1641 TAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCAC 1700
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaG 320

Qy       1701 AAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCG 1760
              |||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |
Db        320 lnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340

Qy       1761 AACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTC 1820
              ||||||||   ||||||||||||||||   ||||||||||||||||||||||||||||||
Db        340 luGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheG 360

Qy       1821 AACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCT 1880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        360 lnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAla 379

Qy       1881 GACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCAT 1939
              |||||||||||||||||||||||||   |||   |||||||||||||||   ||||||
Db        380 AspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHis 399

Qy       1940 CTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTAT 1999
              |||||||||||||||||||||||||||||   |||   |||||||||||||| ||||||
Db        400 LeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIl 419

Qy       2000 ATTTCAATATGGAAAAAAAAAAANAAAAA 2027
              |:::||||||   |||:::|||   :::
Db        419 eTyrGlnTyrGluLysGluLysAlaGlu 428

RESULT 12
US-09-339-338-181
; Sequence 181, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
;  APPLICANT: Yuqiu, Jiang
;  APPLICANT: Dillon, Davin C.
;  APPLICANT: Mitcham, Jennifer L.
;  APPLICANT: Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
;  TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.470C2
;  CURRENT APPLICATION NUMBER: US/09/339,338A
;  CURRENT FILING DATE: 1999-06-23
;  NUMBER OF SEQ ID NOS: 315
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 181
;   LENGTH: 432
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-339-338-181

Alignment Scores:
Pred. No.:              1.17e-182       Length:         432
Score:                  2017.00         Matches:        412
Percent Similarity:     96.06%          Conservative:   3
Best Local Similarity:  95.37%          Mismatches:     13
Query Match:            59.27%          Indels:         5
DB:                     4               Gaps:           0

US-09-602-362E-15 (1-2030) x US-09-339-338-181 (1-432)

Qy        741 GATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCACTGTGAACAACGT 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20

Qy        801 ACAGGAAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAGAAACTGTCAGAA 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGlu 40
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Qy       861 GCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGC 920
Db        41 AlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCys 60

Qy       921 AGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCCGATATATTAAAT 980
Db        61 SerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAlaAspIleLeuAsn 80

Qy       981 GAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAAGAGTTAGAAGTG 1040
Db        81 GluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluVal 100

Qy      1041 AAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAGAGTGTAGAAAGT 1100
Db       101 LysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSer 120

Qy      1101 AATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGC 1160
Db       121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140

Qy      1161 ATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATAC 1220
Db       141 MetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyr 160

Qy      1221 CAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAA 1280
Db       161 GlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGlu 180

Qy      1281 CTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGT 1340
Db       181 LeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSer 200

Qy      1341 GGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAA 1400
Db       201 GlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220

Qy      1401 CAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCT 1460
Db       221 GlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAla 240

Qy      1461 GTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATT 1520
Db       241 ValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIle 260

Qy      1521 GCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAA 1580
Db       261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAs 280

Qy      1581 CAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAAT 1640
Db       280 nAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIl 300

Qy      1641 TAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCAC 1700
Db       300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaG 320

Qy      1701 AAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCG 1760
Db       320 lnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340

Qy      1761 AACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTC 1820
Db       340 luGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheG 360

Qy      1821 AACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCT 1880
Db       360 lnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAla 379

Qy      1881 GACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCAT 1939
Db       380 AspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHis 399

Qy      1940 CTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTAT 1999
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Db        400 LeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIl 419

Qy       2000 ATTTCAATATGGAAAAAAAAAAANAAAAA 2027
Db        419 eTyrGlnTyrGluLysGluLysAlaGlu 428
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RESULT 13
US-09-433-826B-181
; Sequence 181, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 181
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-433-826B-181

Alignment Scores:

Pred. No.:	1.17e-182	Length:	432
Score:	2017.00	Matches:	412
Percent Similarity:	96.06%	Conservative:	3
Best Local Similarity:	95.37%	Mismatches:	13
Query Match:	59.27%	Indels:	5
DB:	4	Gaps:	0

US-09-602-362E-15 (1-2030) x US-09-433-826B-181 (1-432)

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Qy        741 GATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCACTGTGAACAACGT 800
Db          1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20

Qy        801 ACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAGAAACTGTCAGAA 860
Db         21 ThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGlu 40

Qy        861 GCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGC 920
Db         41 AlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCys 60

Qy        921 AGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCCGATATATTAAAT 980
Db         61 SerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAlaAspIleLeuAsn 80

Qy        981 GAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAAGAGTTAGAAGTG 1040
Db         81 GluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluVal 100

Qy       1041 AAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAGAGTGTAGAAAGT 1100
Db        101 LysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSer 120

Qy       1101 AATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGC 1160
Db        121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140

Qy       1161 ATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATAC 1220
Db        141 MetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyr 160

Qy       1221 CAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAA 1280
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Db        161 GlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGlu 180

Qy       1281 CTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGT 1340
Db        181 LeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSer 200

Qy       1341 GGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAA 1400
Db        201 GlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220

Qy       1401 CAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCT 1460
Db        221 GlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAla 240

Qy       1461 GTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATT 1520
Db        241 ValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIle 260

Qy       1521 GCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAA 1580
Db        261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAs 280

Qy       1581 CAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAAT 1640
Db        280 nAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIl 300

Qy       1641 TAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCAC 1700
Db        300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaG 320

Qy       1701 AAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCG 1760
Db        320 lnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340

Qy       1761 AACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTC 1820
Db        340 luGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheG 360

Qy       1821 AACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCT 1880
Db        360 lnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAla 379

Qy       1881 GACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCAT 1939
Db        380 AspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHis 399

Qy       1940 CTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTAT 1999
Db        400 LeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIl 419

Qy       2000 ATTTCAATATGGAAAAAAAAAANAAAAA 2027
Db        419 eTyrGlnTyrGluLysGluLysAlaGlu 428

RESULT 14
US-09-604-287A-181
; Sequence 181, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C7
;  CURRENT APPLICATION NUMBER: US/09/604,287A
;  CURRENT FILING DATE:  2000-06-22
;  NUMBER OF SEQ ID NOS: 489
;  SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 181
;   LENGTH: 432
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-604-287A-181

Alignment Scores:
Pred. No.:                1.17e-182       Length:          432
Score:                    2017.00         Matches:         412
Percent Similarity:       96.06%          Conservative:    3
Best Local Similarity:    95.37%          Mismatches:      13
Query Match:              59.27%          Indels:          5
DB:                       4               Gaps:            0

US-09-602-362E-15 (1-2030) x US-09-604-287A-181 (1-432)

Qy        741 GATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCACTGTGAACAACGT 800
Db          1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20

Qy        801 ACAGGAAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAGAAACTGTCAGAA 860
Db         21 ThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGlu 40

Qy        861 GCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGC 920
Db         41 AlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCys 60

Qy        921 AGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCCGATATATTAAAT 980
Db         61 SerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAlaAspIleLeuAsn 80

Qy        981 GAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAAGAGTTAGAAGTG 1040
Db         81 GluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluVal 100

Qy       1041 AAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAGAGTGTAGAAAGT 1100
Db        101 LysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSer 120

Qy       1101 AATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGC 1160
Db        121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140

Qy       1161 ATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATAC 1220
Db        141 MetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyr 160

Qy       1221 CAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAA 1280
Db        161 GlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGlu 180

Qy       1281 CTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGT 1340
Db        181 LeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSer 200

Qy       1341 GGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAA 1400
Db        201 GlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220

Qy       1401 CAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCT 1460
Db        221 GlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAla 240

Qy       1461 GTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATT 1520
Db        241 ValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIle 260

Qy       1521 GCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAA 1580
Db        261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAs 280

Qy       1581 CAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAAT 1640
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Db        280 nAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIl 300

Qy       1641 TAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCAC 1700
Db        300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaG 320

Qy       1701 AAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCG 1760
Db        320 lnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340

Qy       1761 AACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTC 1820
Db        340 luGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheG 360

Qy       1821 AACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCT 1880
Db        360 lnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAla 379

Qy       1881 GACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCAT 1939
Db        380 AspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHis 399

Qy       1940 CTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTAT 1999
Db        400 LeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIl 419

Qy       2000 ATTTCAATATGGAAAAAAAAAANAAAAA 2027
Db        419 eTyrGlnTyrGluLysGluLysAlaGlu 428

RESULT 15
US-09-285-480-181
; Sequence 181, Application US/09285480
; Patent No. 6590076
; GENERAL INFORMATION:
;  APPLICANT: Yuqui, Jiang
;  APPLICANT: Dillon, Davin C.
;  APPLICANT: Mitcham, Jennifer L.
;  APPLICANT: Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
;  TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.470C1
;  CURRENT APPLICATION NUMBER: US/09/285,480
;  CURRENT FILING DATE: 1999-04-02
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 181
;   LENGTH: 432
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-285-480-181

Alignment Scores:
Pred. No.:              1.17e-182       Length:         432
Score:                  2017.00         Matches:        412
Percent Similarity:     96.06%          Conservative:   3
Best Local Similarity:  95.37%          Mismatches:     13
Query Match:            59.27%          Indels:         5
DB:                     4               Gaps:           0

US-09-602-362E-15 (1-2030) x US-09-285-480-181 (1-432)

Qy        741 GATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCACTGTGAACAACGT 800
Db          1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20

Qy        801 ACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAGAAACTGTCAGAA 860
Db         21 ThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGlu 40

Qy        861 GCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGC 920

Db         41 AlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCys 60

Qy        921 AGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCCGATATATTAAAT 980
Db         61 SerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAlaAspIleLeuAsn 80

Qy        981 GAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAAGAGTTAGAAGTG 1040
Db         81 GluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluVal 100

Qy       1041 AAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAGAGTGTAGAAAGT 1100
Db        101 LysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSer 120

Qy       1101 AATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGC 1160
Db        121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140

Qy       1161 ATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATAC 1220
Db        141 MetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyr 160

Qy       1221 CAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAA 1280
Db        161 GlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGlu 180

Qy       1281 CTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGT 1340
Db        181 LeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSer 200

Qy       1341 GGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAA 1400
Db        201 GlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220

Qy       1401 CAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCT 1460
Db        221 GlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAla 240

Qy       1461 GTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATT 1520
Db        241 ValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIle 260

Qy       1521 GCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAA 1580
Db        261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAs 280

Qy       1581 CAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAAT 1640
Db        280 nAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIl 300

Qy       1641 TAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCAC 1700
Db        300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaG 320

Qy       1701 AAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCG 1760
Db        320 lnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340

Qy       1761 AACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTC 1820
Db        340 luGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheG 360

Qy       1821 AACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCT 1880
Db        360 lnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAla 379

Qy       1881 GACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCAT 1939
Db        380 AspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHis 399

Qy       1940 CTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTAT 1999
Db        400 LeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIl 419
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Qy       2000 ATTTCAATATGGAAAAAAAAAANAAAAA 2027
              |:::|||||   |||:::|||   :::
Db        419 eTyrGlnTyrGluLysGluLysAlaGlu 428
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RESULT 16
US-09-834-759-181
; Sequence 181, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 181
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-834-759-181

Alignment Scores:

Pred. No.:	1.17e-182	Length:	432
Score:	2017.00	Matches:	412
Percent Similarity:	96.06%	Conservative:	3
Best Local Similarity:	95.37%	Mismatches:	13
Query Match:	59.27%	Indels:	5
DB:	4	Gaps:	0

US-09-602-362E-15 (1-2030) x US-09-834-759-181 (1-432)

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Qy        741 GATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCACTGTGAACAACGT 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20

Qy        801 ACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAGAAACTGTCAGAA 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGlu 40

Qy        861 GCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGC 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 AlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCys 60

Qy        921 AGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCCGATATATTAAAT 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAlaAspIleLeuAsn 80

Qy        981 GAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAAGAGTTAGAAGTG 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 GluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluVal 100

Qy       1041 AAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAGAGTGTAGAAAGT 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSer 120

Qy       1101 AATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGC 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140

Qy       1161 ATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATAC 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 MetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyr 160

Qy       1221 CAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAA 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGlu 180

Qy       1281 CTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGT 1340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSer 200

Qy       1341 GGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAA 1400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220

Qy       1401 CAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCT 1460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 GlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAla 240

Qy       1461 GTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATT 1520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIle 260

Qy       1521 GCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAA 1580
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAs 280

Qy       1581 CAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAAT 1640
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        280 nAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIl 300

Qy       1641 TAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCAC 1700
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaG 320

Qy       1701 AAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCG 1760
              |||||||||||||||||||||||||||||||||||||||||||||||||||   |||  |
Db        320 lnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340

Qy       1761 AACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTC 1820
              |||||||  ||||||||||||||  |||||||||||||||||||||||||||||||||||
Db        340 luGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheG 360

Qy       1821 AACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCT 1880
              |||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db        360 lnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAla 379

Qy       1881 GACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCAT 1939
              |||||||||||||||||||||||||  |||  |||||||||||||||  ||||||||||
Db        380 AspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHis 399

Qy       1940 CTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTAT 1999
              |||||||||||||||||||||||||||  |||  |||||||||||||||  ||||||||||
Db        400 LeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIl 419

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Qy       2000 ATTTCAATATGGAAAAAAAAAANAAAAA 2027
              |:::|||||   |||:::|||   :::
Db        419 eTyrGlnTyrGluLysGluLysAlaGlu 428
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RESULT 17
US-09-620-405B-469
; Sequence 469, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 469
;   LENGTH: 650
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(650)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-620-405B-469

Alignment Scores:
Pred. No.:              7.11e-143      Length:          650
Score:                  1597.50        Matches:         321
Percent Similarity:     83.42%         Conservative:    1
Best Local Similarity:  83.16%         Mismatches:      2
Query Match:            46.94%         Indels:          62
DB:                     4              Gaps:            1

US-09-602-362E-15 (1-2030) x US-09-620-405B-469 (1-650)

Qy          9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 346

Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 366

Qy        129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 386

Qy        189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 406

Qy        249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 426

Qy        309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 446

Qy        369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 466

Qy        429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 486

Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 506

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        507 ThrLeuArgAlaAspGlnMetProSerGluSerLysGlnLys***ValGluGluAsn 526

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 546

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 566

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 586

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 606

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 626

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
              ||||||||||||||||||
Db        627 GlnGluLeuCysSerVal---------------------------------------- 632

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028

Db        632 ------------------------------------------------------------ 632

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088

Db        632 ------------------------------------------------------------ 632

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
                                      ::: ||||||||||||||||||||||||||||||||
Db        633 ---------------------Arg-PheLeuThrLeuMetLysMetLysIleIleSerTy 645

Qy       1149 CATGAAAATTGCATGT 1164
              ||||||||||||||||
Db        645 rMetLysIleAlaCys 650

RESULT 18
US-09-433-826B-469
; Sequence 469, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE:  210121.470C4
;  CURRENT APPLICATION NUMBER: US/09/433,826B
;  CURRENT FILING DATE:  1999-11-03
;  NUMBER OF SEQ ID NOS:  474
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 469
;   LENGTH: 650
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (310)
;   NAME/KEY: Xaa = Any Amino Acid<221> unsure
;   LOCATION: (429)
;   NAME/KEY: Xaa = Any Amino Acid<221> unsure
;   LOCATION: (522)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-433-826B-469

Alignment Scores:
Pred. No.:              7.11e-143      Length:          650
Score:                  1597.50        Matches:         321
Percent Similarity:     83.42%         Conservative:    1
Best Local Similarity:  83.16%         Mismatches:      2
Query Match:            46.94%         Indels:          62
DB:                     4              Gaps:            1

US-09-602-362E-15 (1-2030) x US-09-433-826B-469 (1-650)

Qy          9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 346

Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 366

Qy        129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 386

Qy        189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 406

Qy        249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 426

Qy        309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
                 ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 446

Qy        369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 466

Qy        429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 486

Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 506

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
                 ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        507 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 526

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 546

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 566

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 586

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 606

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 626

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
                 ||||||||||||||||
Db        627 GlnGluLeuCysSerVal---------------------------------------- 632

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028

Db        632 ---------------------------------------------------------- 632

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088

Db        632 ---------------------------------------------------------- 632

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
                              ::: ||||||||||||||||||||||||||||||||||||||
Db        633 ---------------------Arg-PheLeuThrLeuMetLysMetLysIleIleSerTy 645

Qy       1149 CATGAAAATTGCATGT 1164
                 ||||||||||||||||

Db        645 rMetLysIleAlaCys 650

RESULT 19
US-09-604-287A-469
; Sequence 469, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C7
;  CURRENT APPLICATION NUMBER: US/09/604,287A
;  CURRENT FILING DATE:  2000-06-22
;  NUMBER OF SEQ ID NOS: 489
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 469
;   LENGTH: 650
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (310)
;   OTHER INFORMATION: Xaa = Any Amino Acid
;   NAME/KEY: unsure
;   LOCATION: (429)
;   OTHER INFORMATION: Xaa = Any Amino Acid
;   NAME/KEY: unsure
;   LOCATION: (522)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-604-287A-469

Alignment Scores:
Pred. No.:                7.11e-143       Length:          650
Score:                    1597.50         Matches:         321
Percent Similarity:       83.42%          Conservative:    1
Best Local Similarity:    83.16%          Mismatches:      2
Query Match:              46.94%          Indels:          62
DB:                       4               Gaps:            1

US-09-602-362E-15 (1-2030) x US-09-604-287A-469 (1-650)

Qy          9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 346

Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 366

Qy        129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 386

Qy        189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 406

Qy        249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 426

Qy        309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
                 ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 446

Qy        369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 466
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Qy        429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 486

Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 506

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 526

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 546

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 566

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 586

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 606

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 626

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
              ||||||||||||||||||
Db        627 GlnGluLeuCysSerVal---------------------------------------- 632

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028

Db        632 ------------------------------------------------------------ 632

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088

Db        632 ------------------------------------------------------------ 632

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
                                  ::: ||||||||||||||||||||||||||||||||||
Db        633 ---------------------Arg-PheLeuThrLeuMetLysMetLysIleIleSerTy 645

Qy       1149 CATGAAAATTGCATGT 1164
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Db        645 rMetLysIleAlaCys 650

RESULT 20
US-09-834-759-469
; Sequence 469, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C9
;  CURRENT APPLICATION NUMBER: US/09/834,759
;  CURRENT FILING DATE:  2001-04-13
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 469
;  LENGTH: 650
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: unsure
;  LOCATION: (310)
;  OTHER INFORMATION: Xaa = Any Amino Acid
;  NAME/KEY: unsure
;  LOCATION: (429)
;  OTHER INFORMATION: Xaa = Any Amino Acid
;  NAME/KEY: unsure
;  LOCATION: (522)
;  OTHER INFORMATION: Xaa = Any Amino Acid
US-09-834-759-469

Alignment Scores:
Pred. No.:                7.11e-143      Length:          650
Score:                    1597.50        Matches:         321
Percent Similarity:       83.42%         Conservative:    1
Best Local Similarity:    83.16%         Mismatches:      2
Query Match:              46.94%         Indels:          62
DB:                       4              Gaps:            1

US-09-602-362E-15 (1-2030) x US-09-834-759-469 (1-650)

Qy          9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 346

Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 366

Qy        129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 386

Qy        189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 406

Qy        249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 426

Qy        309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 446

Qy        369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 466

Qy        429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 486

Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 506

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 526

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 546

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 566
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Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 586

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 606

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 626

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
              ||||||||||||||||
Db        627 GlnGluLeuCysSerVal---------------------------------------- 632

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028

Db        632 ---------------------------------------------------------- 632

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088

Db        632 ---------------------------------------------------------- 632

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
                                  ::: ||||||||||||||||||||||||||||||||||
Db        633 --------------------Arg-PheLeuThrLeuMetLysMetLysIleIleSerTy 645

Qy       1149 CATGAAAATTGCATGT 1164
              ||||||||||||||||
Db        645 rMetLysIleAlaCys 650
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RESULT 21
US-09-620-405B-494
; Sequence 494, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 494
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(743)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-620-405B-494

Alignment Scores:

Pred. No.:	7.44e-143	Length:	743
Score:	1597.50	Matches:	321
Percent Similarity:	83.42%	Conservative:	1
Best Local Similarity:	83.16%	Mismatches:	2
Query Match:	46.94%	Indels:	62
DB:	4	Gaps:	1

US-09-602-362E-15 (1-2030) x US-09-620-405B-494 (1-743)

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Qy          9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 439

Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 459

Qy        129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 479

Qy        189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 499

Qy        249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 519

Qy        309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
              ||||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 539

Qy        369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 559

Qy        429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 579

Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 599

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 619

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 639

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 659

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 679

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 699

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 719

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
              ||||||||||||||||
Db        720 GlnGluLeuCysSerVal---------------------------------------- 725

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028

Db        725 ---------------------------------------------------------- 725

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088

Db        725 ---------------------------------------------------------- 725

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
                                  ::: ||||||||||||||||||||||||||||||||||
Db        726 --------------------Arg-PheLeuThrLeuMetLysMetLysIleIleSerTy 738
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Qy       1149 CATGAAAATTGCATGT 1164
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Db        738 rMetLysIleAlaCys 743

RESULT 22
US-09-834-759-494
; Sequence 494, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C9
;  CURRENT APPLICATION NUMBER: US/09/834,759
;  CURRENT FILING DATE:  2001-04-13
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 494
;   LENGTH: 743
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: variant
;   LOCATION: (1)...(743)
;   OTHER INFORMATION: Xaa = Any amino acid
US-09-834-759-494

Alignment Scores:
Pred. No.:              7.44e-143     Length:          743
Score:                  1597.50       Matches:         321
Percent Similarity:     83.42%        Conservative:    1
Best Local Similarity:  83.16%        Mismatches:      2
Query Match:            46.94%        Indels:          62
DB:                     4             Gaps:            1

US-09-602-362E-15 (1-2030) x US-09-834-759-494 (1-743)

Qy          9 GTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 439

Qy         69 TTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 459

Qy        129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAA 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 479

Qy        189 CAAACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAA 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 499

Qy        249 AGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCC 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 519

Qy        309 AAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGAT 368
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 539

Qy        369 AATGATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 559

Qy        429 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        560 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 579

Qy        489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 599

Qy        549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAAT 608
              ||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        600 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 619

Qy        609 TCTTGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAG 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 639

Qy        669 GCTACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 659

Qy        729 TCAAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCAC 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 679

Qy        789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAG 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 699

Qy        849 AAACTGTCAGAAGCAAAAGAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAA 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 719

Qy        909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCC 968
              ||||||||||||||||
Db        720 GlnGluLeuCysSerVal---------------------------------------- 725

Qy        969 GATATATTAAATGAAAAAATTAGGGAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAA 1028

Db        725 ---------------------------------------------------------- 725

Qy       1029 GAGTTAGAAGTGAAACAACAACTTGAACAGGCTCTCAGAATACAAGATATAGAATTGAAG 1088

Db        725 ---------------------------------------------------------- 725

Qy       1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTA 1148
                                          ::: ||||||||||||||||||||||||||||||
Db        726 --------------------Arg-PheLeuThrLeuMetLysMetLysIleIleSerTy 738

Qy       1149 CATGAAAATTGCATGT 1164
              ||||||||||||||||
Db        738 rMetLysIleAlaCys 743

RESULT 23
US-09-620-405B-495
; Sequence 495, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C8
;  CURRENT APPLICATION NUMBER: US/09/620,405B
;  CURRENT FILING DATE:  2000-07-20
;  NUMBER OF SEQ ID NOS: 495
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 495
;   LENGTH: 410
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-620-405B-495
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Alignment Scores:
Pred. No.:              1.14e-124      Length:          410
Score:                  1404.50        Matches:         300
Percent Similarity:     82.85%         Conservative:    14
Best Local Similarity:  79.16%         Mismatches:      50
Query Match:            41.27%         Indels:          16
DB:                     4              Gaps:            1

US-09-602-362E-15 (1-2030) x US-09-620-405B-495 (1-410)

Qy       933 ACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCCGATATATTAAATGAAAAAATTAGG 992
             |||:::|||   :::      |||           ::::::|||   |||   |||
Db        32 ThrIleAsnProGlnValSerLysThrGluTyrLysGluLeuLeuGlnGluPheIleAsp 51

Qy       993 GAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAAGAGTTAGAAGTGAAACAACAACTT 1052
             :::                    ||||||      :::   |||
Db        52 AspAsnAlaThrThrAsnAlaIleAspGluLeuLysGluCysPheLeuAsnGlnThrAsp 71

Qy       1053 GAACAGGCTCTCAGAATACAAGATATAGAATTGAAGAGTGTAGAAAGTAATTTG------ 1106
              |||          ::::::                 :::|||:::|||
Db         72 GluThrLeuSerAsnValGluValPheMetGlnLeuIleTyrAspSerSerLeuCysAsp 91

Qy       1107 --------------------------AATCAGGTTTCTCACACTCATGAAAATGAAAAT 1139
                                        :::|||||||||||||||||||||||||||||
Db         92 LeuPheMetGlyThrArgAlaLeuGlnCysGluValSerHisThrHisGluAsnGluAsn 111

Qy       1140 TATCTCTTACATGAAAATTGCATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATA 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 TyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIle 131

Qy       1200 GCCACACTGAAACACCAATACCAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 AlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIle 151

Qy       1260 TTAAAAGAAAAGAATGCTGAACTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 LeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThr 171

Qy       1320 AAAAGGGCATCTCAATATAGTGGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTC 1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 LysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeu 191

Qy       1380 ACTTCTAAATTGAAGGAAAAACAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACAC 1439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 ThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHis 211

Qy       1440 CATCCTAGACTGGCTTCTGCTGTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGT 1499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 HisProArgLeuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSer 231

Qy       1500 CAAGAACCTGCTTTCCACATTGCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGAT 1559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 GlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAsp 251

Qy       1560 GTGAGTAGTACCGATATATAACAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAG 1619
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ValSerSerThr-IleTyrAsnAsnGluValLeuHisGlnProLeuSerGluAlaGlnAr 271

Qy       1620 GAAATCCANAAGCCTAAAAATTAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATAC 1679
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 gLysSerLysSerLeuLysIleAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnTh 291

Qy       1680 ATTGGTTTCAGGAACATGCACAAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAG 1739
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 rLeuValSer-GluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLysGluA 311

Qy       1740 CTGAACACATGTNTCAAANCGAACAAGATNATGTGAACAAACACACTGANCAGCAGGAGT 1799
              |||||||||||   |||   |||||||||   |||||||||||||||   ||||||||||
Db        311 laGluHisMetTyrGlnAsnGluGlnAspAsnValAsnLysHisThrGluGlnGlnGluS 331

Qy       1800 CTCTAGATCAGAAATTATTTCAACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAG 1859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        331 erLeuAspGlnLysLeuPheGlnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuV 351

Qy       1860 TTCATGCACATAANGAAAGCTGACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTT 1919
              ||||||||||||   ||||||||||||||||||||||||||||||||||||   |||   |||
Db        351 alHisAlaHis-LysLysAlaAspAsnLysSerLysIleThrIleAspIleHisPheLeu 370

Qy       1920 GAGAGGAAAATGCN-CATCATCTTCTAAAAGAGAAAAAATGAGGAGATATTTNATTACNAT 1978
              ||||||||||||   ||||||||||||||||||||||||||||||||||||   |||
Db        371 GluArgLysMetGlnHisHisLeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsn 390

Qy       1979 AACCATTTAAAAAAACCCGTATATTTCAATATGGAAAAAAAAAAANAAAAA 2027
              |||||||||||||| ||||||:::||||||   |||:::|||   :::
Db        391 AsnHisLeuLysAsn-ArgIleTyrGlnTyrGluLysGluLysAlaGlu 406

RESULT 24
US-09-834-759-495
; Sequence 495, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C9
;  CURRENT APPLICATION NUMBER: US/09/834,759
;  CURRENT FILING DATE:  2001-04-13
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 495
;   LENGTH: 410
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-759-495

Alignment Scores:
Pred. No.:              1.14e-124      Length:          410
Score:                  1404.50        Matches:         300
Percent Similarity:     82.85%         Conservative:    14
Best Local Similarity:  79.16%         Mismatches:      50
Query Match:            41.27%         Indels:          16
DB:                     4              Gaps:            1

US-09-602-362E-15 (1-2030) x US-09-834-759-495 (1-410)

Qy       933 ACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCCGATATATTAAATGAAAAAATTAGG 992
             |||:::|||   :::      |||           ::::::|||   |||   |||
Db        32 ThrIleAsnProGlnValSerLysThrGluTyrLysGluLeuLeuGlnGluPheIleAsp 51

Qy       993 GAAGAATTAGGAAGAATCGAAGAGCAGCATAGGAAAGAGTTAGAAGTGAAACAACAACTT 1052
             :::                    ||||||      :::   |||
Db        52 AspAsnAlaThrThrAsnAlaIleAspGluLeuLysGluCysPheLeuAsnGlnThrAsp 71

Qy       1053 GAACAGGCTCTCAGAATACAAGATATAGAATTGAAGAGTGTAGAAAGTAATTTG------ 1106
              |||          ::::::                 :::|||:::|||
Db         72 GluThrLeuSerAsnValGluValPheMetGlnLeuIleTyrAspSerSerLeuCysAsp 91

Qy       1107 --------------------------AATCAGGTTTCTCACACTCATGAAAATGAAAAT 1139
                                        :::|||||||||||||||||||||||||||||
Db         92 LeuPheMetGlyThrArgAlaLeuGlnCysGluValSerHisThrHisGluAsnGluAsn 111

Qy       1140 TATCTCTTACATGAAAATTGCATGTTGAAAAAGGAAATTGCCATGCTAAAACTGGAAATA 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 TyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIle 131

Qy       1200 GCCACACTGAAACACCAATACCAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 AlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIle 151
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Qy       1260 TTAAAAGAAAAGAATGCTGAACTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACT 1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 LeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThr 171

Qy       1320 AAAAGGGCATCTCAATATAGTGGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTC 1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 LysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeu 191

Qy       1380 ACTTCTAAATTGAAGGAAAAACAAGACAAAGAAATACTAGAGGCAGAAATTGAATCACAC 1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 ThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHis 211

Qy       1440 CATCCTAGACTGGCTTCTGCTGTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGT 1499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 HisProArgLeuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSer 231

Qy       1500 CAAGAACCTGCTTTCCACATTGCAGGAGATGCTTGTTTGCAAAGAAAAATGAATGTTGAT 1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 GlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAsp 251

Qy       1560 GTGAGTAGTACCGATATATAACAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAG 1619
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ValSerSerThr-IleTyrAsnAsnGluValLeuHisGlnProLeuSerGluAlaGlnAr 271

Qy       1620 GAAATCCANAAGCCTAAAAATTAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATAC 1679
             |||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 gLysSerLysSerLeuLysIleAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnTh 291

Qy       1680 ATTGGTTTCAGGAACATGCACAAAGAGACCAACGTGAAACACAGTGTCAAATGAAGGAAG 1739
             |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 rLeuValSer-GluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLysGluA 311

Qy       1740 CTGAACACATGTNTCAAANCGAACAAGATNATGTGAACAAACACACTGANCAGCAGGAGT 1799
             |||||||||||   |||  |||||||||   |||||||||||||||   ||||||||||
Db        311 laGluHisMetTyrGlnAsnGluGlnAspAsnValAsnLysHisThrGluGlnGlnGluS 331

Qy       1800 CTCTAGATCAGAAATTATTTCAACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAG 1859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 erLeuAspGlnLysLeuPheGlnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuV 351

Qy       1860 TTCATGCACATAANGAAAGCTGACAACAAAAGCAAGATAACAATTGATNTTCATTNTCTT 1919
             ||||||||||   |||||||||||||||||||||||||||||||   |||   |||
Db        351 alHisAlaHis-LysLysAlaAspAsnLysSerLysIleThrIleAspIleHisPheLeu 370

Qy       1920 GAGAGGAAAATGCN-CATCATCTTCTAAAAGAGAAAAATGAGGAGATATTTNATTACNAT 1978
             ||||||||||||   |||||||||||||||||||||||||||||||   |||
Db        371 GluArgLysMetGlnHisHisLeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsn 390

Qy       1979 AACCATTTAAAAAACCCGTATATTTCAATATGGAAAAAAAAAANAAAAA 2027
             ||||||||||||||| |||||:::|||||   |||:::|||   :::
Db        391 AsnHisLeuLysAsn-ArgIleTyrGlnTyrGluLysGluLysAlaGlu 406
```

RESULT 25
US-09-389-681-176
; Sequence 176, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-389-681-176

Alignment Scores:

Pred. No.:	5.38e-124	Length:	317
Score:	1397.00	Matches:	288
Percent Similarity:	94.50%	Conservative:	4
Best Local Similarity:	93.20%	Mismatches:	13
Query Match:	41.05%	Indels:	5
DB:	4	Gaps:	0

US-09-602-362E-15 (1-2030) x US-09-389-681-176 (1-317)

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Qy       1110 CAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGTTGAAA 1169
                 :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys 28

Qy       1170 AAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAAG 1229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48

Qy       1230 GAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAACTTCAGATG 1289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68

Qy       1290 ACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTT 1349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88

Qy       1350 AAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAA 1409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108

Qy       1410 GAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGAC 1469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128

Qy       1470 CATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGAT 1529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148

Qy       1530 GCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVa 168

Qy       1590 GCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAATTAATCTCAA 1649
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        168 lLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188

Qy       1650 TTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCACAAAGAGACC 1709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208

Qy       1710 AACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGATN 1769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 lnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228

Qy       1770 ATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAA 1829
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248

Qy       1830 GCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGACAACAAA 1889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 erLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267

Qy       1890 AGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAAA 1948
              ||||||||||||||||   |||   |||||||||||||||||   ||||||||||||||
Db        268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHisLeuLeuLys 287

Qy       1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTATATTTCAATA 2008
              ||||||||||||||||||   |||   |||||||||||||| ||||||:::|||||
Db        288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307

Qy       2009 TGGAAAAAAAAAAANAAAAA 2027
              |   |||:::|||   :::
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```
Db        307 rGluLysGluLysAlaGlu 313

RESULT 26
US-09-620-405B-176
; Sequence 176, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C8
;  CURRENT APPLICATION NUMBER: US/09/620,405B
;  CURRENT FILING DATE:  2000-07-20
;  NUMBER OF SEQ ID NOS: 495
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 176
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-620-405B-176

Alignment Scores:
Pred. No.:              5.38e-124      Length:          317
Score:                  1397.00        Matches:         288
Percent Similarity:     94.50%         Conservative:    4
Best Local Similarity:  93.20%         Mismatches:      13
Query Match:            41.05%         Indels:          5
DB:                     4              Gaps:            0

US-09-602-362E-15 (1-2030) x US-09-620-405B-176 (1-317)

Qy       1110 CAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGTTGAAA 1169
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys 28

Qy       1170 AAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAAG 1229
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48

Qy       1230 GAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAACTTCAGATG 1289
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68

Qy       1290 ACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTT 1349
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88

Qy       1350 AAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAA 1409
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108

Qy       1410 GAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGAC 1469
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128

Qy       1470 CATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGAT 1529
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148

Qy       1530 GCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVa 168

Qy       1590 GCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAATTAATCTCAA 1649
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 lLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188

Qy       1650 TTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCACAAAGAGACC 1709
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208

Qy       1710 AACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGATN 1769
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 lnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228

Qy       1770 ATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAA 1829
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248

Qy       1830 GCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGACAACAAA 1889
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 erLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267

Qy       1890 AGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAAA 1948
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHisLeuLeuLys 287

Qy       1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTATATTTCAATA 2008
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307

Qy       2009 TGGAAAAAAAAAAANAAAAA 2027
              |  |||:::|||   :::
Db        307 rGluLysGluLysAlaGlu 313

RESULT 27
US-09-339-338-176
; Sequence 176, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
;  APPLICANT: Yuqiu, Jiang
;  APPLICANT: Dillon, Davin C.
;  APPLICANT: Mitcham, Jennifer L.
;  APPLICANT: Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
;  TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.470C2
;  CURRENT APPLICATION NUMBER: US/09/339,338A
;  CURRENT FILING DATE: 1999-06-23
;  NUMBER OF SEQ ID NOS: 315
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 176
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-339-338-176

Alignment Scores:
Pred. No.:              5.38e-124      Length:          317
Score:                  1397.00        Matches:         288
Percent Similarity:     94.50%         Conservative:    4
Best Local Similarity:  93.20%         Mismatches:      13
Query Match:            41.05%         Indels:          5
DB:                     4              Gaps:            0

US-09-602-362E-15 (1-2030) x US-09-339-338-176 (1-317)

Qy       1110 CAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGTTGAAA 1169
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys 28

Qy       1170 AAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAAG 1229
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48

Qy       1230 GAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAACTTCAGATG 1289
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68

Qy       1290 ACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTT 1349
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88

Qy       1350 AAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAA 1409
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108

Qy       1410 GAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGAC 1469
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128

Qy       1470 CATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGAT 1529
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148

Qy       1530 GCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVa 168

Qy       1590 GCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAATTAATCTCAA 1649
              |||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        168 lLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188

Qy       1650 TTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCACAAAGAGACC 1709
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208

Qy       1710 AACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGATN 1769
              |||||||||||||||||||||||||||||||||||||||||||||||   |||   |||||||||
Db        208 lnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228

Qy       1770 ATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAA 1829
                |||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||
Db        228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248

Qy       1830 GCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGACAACAAA 1889
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 erLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267

Qy       1890 AGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAAA 1948
              |||||||||||||||||||   |||   |||||||||||||||   |||||||||||||||||
Db        268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHisLeuLeuLys 287

Qy       1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTATATTTCAATA 2008
              |||||||||||||||||||   |||   |||||||||||||||||||:::|||||
Db        288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307

Qy       2009 TGGAAAAAAAAAAANAAAAA 2027
              |   |||:::|||   :::
Db        307 rGluLysGluLysAlaGlu 313

RESULT 28
US-09-433-826B-176
; Sequence 176, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE:  210121.470C4
;  CURRENT APPLICATION NUMBER: US/09/433,826B
;  CURRENT FILING DATE:  1999-11-03
;  NUMBER OF SEQ ID NOS:  474
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 176
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-433-826B-176
```

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Alignment Scores:
Pred. No.:                5.38e-124      Length:          317
Score:                    1397.00        Matches:         288
Percent Similarity:       94.50%         Conservative:    4
Best Local Similarity:    93.20%         Mismatches:      13
Query Match:              41.05%         Indels:          5
DB:                       4              Gaps:            0

US-09-602-362E-15 (1-2030) x US-09-433-826B-176 (1-317)

Qy       1110 CAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGTTGAAA 1169
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys 28

Qy       1170 AAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAAG 1229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48

Qy       1230 GAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAACTTCAGATG 1289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68

Qy       1290 ACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTT 1349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88

Qy       1350 AAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAA 1409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108

Qy       1410 GAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGAC 1469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128

Qy       1470 CATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGAT 1529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148

Qy       1530 GCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVa 168

Qy       1590 GCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAATTAATCTCAA 1649
              |||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        168 lLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188

Qy       1650 TTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCACAAAGAGACC 1709
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208

Qy       1710 AACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGATN 1769
              |||||||||||||||||||||||||||||||||||||||||||||||   |||   |||||||||
Db        208 lnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228

Qy       1770 ATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAA 1829
                |||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||
Db        228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248

Qy       1830 GCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGACAACAAA 1889
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 erLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267

Qy       1890 AGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAAA 1948
              |||||||||||||||||||   |||   |||||||||||||||   |||||||||||||||||
Db        268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHisLeuLeuLys 287

Qy       1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTATATTTCAATA 2008
              |||||||||||||||||||   |||   |||||||||||||||||||:::|||||
Db        288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307

Qy       2009 TGGAAAAAAAAAAANAAAAA 2027
              |   |||:::|||   :::
Db        307 rGluLysGluLysAlaGlu 313
```

```
RESULT 29
US-09-604-287A-176
; Sequence 176, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C7
;  CURRENT APPLICATION NUMBER: US/09/604,287A
;  CURRENT FILING DATE:  2000-06-22
;  NUMBER OF SEQ ID NOS: 489
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 176
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-604-287A-176

Alignment Scores:
Pred. No.:              5.38e-124       Length:         317
Score:                  1397.00         Matches:        288
Percent Similarity:     94.50%          Conservative:   4
Best Local Similarity:  93.20%          Mismatches:     13
Query Match:            41.05%          Indels:         5
DB:                     4               Gaps:           0

US-09-602-362E-15 (1-2030) x US-09-604-287A-176 (1-317)

Qy       1110 CAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGTTGAAA 1169
                 :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db             9 GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys 28

Qy       1170 AAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAAG 1229
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48

Qy       1230 GAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAACTTCAGATG 1289
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68

Qy       1290 ACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTT 1349
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88

Qy       1350 AAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAA 1409
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108

Qy       1410 GAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGAC 1469
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128

Qy       1470 CATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGAT 1529
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148

Qy       1530 GCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
                 |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db           149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVa 168

Qy       1590 GCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAATTAATCTCAA 1649
                 ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db           168 lLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188

Qy       1650 TTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCACAAAGAGACC 1709
                 |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||

Db           188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208

Qy       1710 AACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGATN 1769
                 ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||||||||
Db           208 lnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228

Qy       1770 ATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAA 1829
                   ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db           228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248

Qy       1830 GCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGACAACAAA 1889
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           248 erLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267

Qy       1890 AGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAAA 1948
                 ||||||||||||||||||   |||   ||||||||||||||   ||||||||||||||||
Db           268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHisLeuLeuLys 287

Qy       1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTATATTTCAATA 2008
                 ||||||||||||||||||||   |||   |||||||||||||| ||||||:::|||||
Db           288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307

Qy       2009 TGGAAAAAAAAAAANAAAAA 2027
                 |   |||:::|||   :::
Db           307 rGluLysGluLysAlaGlu 313

RESULT 30
US-09-285-480-176
; Sequence 176, Application US/09285480
; Patent No. 6590076
; GENERAL INFORMATION:
;  APPLICANT: Yuqui, Jiang
;  APPLICANT: Dillon, Davin C.
;  APPLICANT: Mitcham, Jennifer L.
;  APPLICANT: Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
;  TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.470C1
;  CURRENT APPLICATION NUMBER: US/09/285,480
;  CURRENT FILING DATE: 1999-04-02
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 176
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-285-480-176

Alignment Scores:
Pred. No.:              5.38e-124       Length:         317
Score:                  1397.00         Matches:        288
Percent Similarity:     94.50%          Conservative:   4
Best Local Similarity:  93.20%          Mismatches:     13
Query Match:            41.05%          Indels:         5
DB:                     4               Gaps:           0

US-09-602-362E-15 (1-2030) x US-09-285-480-176 (1-317)

Qy       1110 CAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGTTGAAA 1169
                 :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db             9 GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys 28

Qy       1170 AAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAAG 1229
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48

Qy       1230 GAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAACTTCAGATG 1289
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68

Qy       1290 ACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTT 1349
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88
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Qy       1350 AAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAA 1409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108

Qy       1410 GAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGAC 1469
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128

Qy       1470 CATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGAT 1529
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148

Qy       1530 GCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVa 168

Qy       1590 GCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAATTAATCTCAA 1649
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         168 lLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188

Qy       1650 TTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCACAAAGAGACC 1709
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208

Qy       1710 AACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGATN 1769
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         208 lnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228

Qy       1770 ATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAA 1829
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248

Qy       1830 GCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGACAACAAA 1889
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         248 erLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267

Qy       1890 AGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAAA 1948
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHisLeuLeuLys 287

Qy       1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTATATTTCAATA 2008
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307

Qy       2009 TGGAAAAAAAAAAANAAAAA 2027
             ||||||||||||||||||||
Db         307 rGluLysGluLysAlaGlu 313
```

RESULT 31
US-09-834-759-176
; Sequence 176, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-834-759-176

Alignment Scores:

Pred. No.:	5.38e-124	Length:	317
Score:	1397.00	Matches:	288
Percent Similarity:	94.50%	Conservative:	4
Best Local Similarity:	93.20%	Mismatches:	13
Query Match:	41.05%	Indels:	5
DB:	4	Gaps:	0

US-09-602-362E-15 (1-2030) x US-09-834-759-176 (1-317)

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Qy       1110 CAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGTTGAAA 1169
             :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           9 GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys 28

Qy       1170 AAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAAG 1229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48

Qy       1230 GAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAACTTCAGATG 1289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68

Qy       1290 ACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTT 1349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88

Qy       1350 AAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAA 1409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108

Qy       1410 GAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGAC 1469
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128

Qy       1470 CATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGAT 1529
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148

Qy       1530 GCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVa 168

Qy       1590 GCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAATTAATCTCAA 1649
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          168 lLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188

Qy       1650 TTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCACAAAGAGACC 1709
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208

Qy       1710 AACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGATN 1769
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          208 lnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228

Qy       1770 ATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAA 1829
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248

Qy       1830 GCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGACAACAAA 1889
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          248 erLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267

Qy       1890 AGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAAA 1948
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHisLeuLeuLys 287

Qy       1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTATATTTCAATA 2008
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307

Qy       2009 TGGAAAAAAAAAAANAAAAA 2027
             ||||||||||||||||||||
```

```
Db        307 rGluLysGluLysAlaGlu 313

RESULT 32
US-09-620-405B-483
; Sequence 483, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C8
;  CURRENT APPLICATION NUMBER: US/09/620,405B
;  CURRENT FILING DATE:  2000-07-20
;  NUMBER OF SEQ ID NOS: 495
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 483
;   LENGTH: 323
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-620-405B-483

Alignment Scores:
Pred. No.:              5.41e-124      Length:          323
Score:                  1397.00        Matches:         288
Percent Similarity:     94.50%         Conservative:    4
Best Local Similarity:  93.20%         Mismatches:      13
Query Match:            41.05%         Indels:          5
DB:                     4              Gaps:            0

US-09-602-362E-15 (1-2030) x US-09-620-405B-483 (1-323)

Qy       1110 CAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGTTGAAA 1169
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys 28

Qy       1170 AAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAAG 1229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48

Qy       1230 GAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAACTTCAGATG 1289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68

Qy       1290 ACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTT 1349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88

Qy       1350 AAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAA 1409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108

Qy       1410 GAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGAC 1469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128

Qy       1470 CATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGAT 1529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148

Qy       1530 GCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVa 168

Qy       1590 GCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAATTAATCTCAA 1649
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        168 lLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188

Qy       1650 TTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCACAAAGAGACC 1709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208

Qy       1710 AACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGATN 1769
              |||||||||||||||||||||||||||||||||||||||||||  |||  |||||||||
Db        208 lnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228

Qy       1770 ATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAA 1829
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248

Qy       1830 GCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGACAACAAA 1889
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        248 erLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267

Qy       1890 AGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAAA 1948
              |||||||||||||||||  |||  ||||||||||||||||  |||||||||||||||||
Db        268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHisLeuLeuLys 287

Qy       1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTATATTTCAATA 2008
              ||||||||||||||||||  |||  |||||||||||||| ||||||:::|||||
Db        288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307

Qy       2009 TGGAAAAAAAAAAANAAAAA 2027
              |   |||:::|||   :::
Db        307 rGluLysGluLysAlaGlu 313

RESULT 33
US-09-604-287A-483
; Sequence 483, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C7
;  CURRENT APPLICATION NUMBER: US/09/604,287A
;  CURRENT FILING DATE:  2000-06-22
;  NUMBER OF SEQ ID NOS: 489
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 483
;   LENGTH: 323
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-604-287A-483

Alignment Scores:
Pred. No.:              5.41e-124      Length:          323
Score:                  1397.00        Matches:         288
Percent Similarity:     94.50%         Conservative:    4
Best Local Similarity:  93.20%         Mismatches:      13
Query Match:            41.05%         Indels:          5
DB:                     4              Gaps:            0

US-09-602-362E-15 (1-2030) x US-09-604-287A-483 (1-323)

Qy       1110 CAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGTTGAAA 1169
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys 28

Qy       1170 AAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAAG 1229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48

Qy       1230 GAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAACTTCAGATG 1289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68
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Qy       2009 TGGAAAAAAAAAAANAAAAA 2027
              |   |||:::|||   :::
Db        307 rGluLysGluLysAlaGlu 313

RESULT 35
US-09-620-405B-472
; Sequence 472, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C8
;  CURRENT APPLICATION NUMBER: US/09/620,405B
;  CURRENT FILING DATE:  2000-07-20
;  NUMBER OF SEQ ID NOS: 495
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 472
;   LENGTH: 466
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(466)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-620-405B-472

Alignment Scores:
Pred. No.:              5.05e-93      Length:          466
Score:                  1070.50       Matches:         216
Percent Similarity:     84.19%        Conservative:    13
Best Local Similarity:  79.41%        Mismatches:      26
Query Match:            31.46%        Indels:          17
DB:                     4             Gaps:            2

US-09-602-362E-15 (1-2030) x US-09-620-405B-472 (1-466)

Qy         12 AAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 71
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        209 LysAspGlyLeuLeuLysAlaThrCysGlyMetLysValSerIleProThrLysAlaLeu 228

Qy         72 GAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAG 131
              ||||||  ||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        229 GluLeuLysAspMetGlnThrPheLysAlaGluProProGlyLysProSerAlaPheGlu 248

Qy        132 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAA 191
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 ProAlaThrGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 268

Qy        192 ACATTGAGAGCAGATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAAAGT 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        269 ThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGluAsn 288

Qy        252 TCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCCAAG 311
              |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        289 SerTrpAspThrGluSerLeuCysGluThrValSerGlnLysAspValCysLeuProLys 308

Qy        312 GCTACACATCAAAAAGAAATAGATAAAATAAATGGAAAATTAGAAGAGTCTCCTGATAAT 371
              |||  ||||||||||||||||||||||||||||||||||||  ||||||
Db        309 AlaAlaHisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGlySerProGlyLys 328

Qy        372 GATGGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTAGAA 431
                 |||   |||||||||   |||   ||||||||||||||||||||||||||||||||
Db        329 ***GlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAlaLeuGlu 348

Qy        432 TTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAGCCT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        349 LeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGluPro 368

Qy        492 GCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAAACA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThr 388

Qy        552 TTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAAGAAGGTTGAAGAAAATTCT 611
              ||||||||||||:::::   ||||||||||||||||||||      ||||||:::|||
Db        389 LeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSer 408

Qy        612 TGGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTACCCAAGGCT 671
              ||||||||||||||||   |||||||||||||||||||||||:::|||||||||
Db        409 TrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuProLysAla 428

Qy        672 ACACATCAAAAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTATCA 731
                 ||||||||||:::|||||||||:::|||||||||||
Db        429 AlaHisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGly--------------- 443

Qy        732 AAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGGAACTTCAAAAAGATCACTGT 791
                                                 :::   |||   |||   |||:::|||
Db        444 ----------------------------LysAsnArgPheLeuPheLysAsnHisLeu 453

Qy        792 GAACAACGTACAGGAAAAATGGAACAAATGAAAAAG 827
                 :::        |||:::      |||:::|||
Db        454 ThrLysTyrPheSerLysLeu------MetArgLys 463

Search completed: July 21, 2004, 08:56:11
Job time : 76.5 secs
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Qy       1290 ACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTT 1349
Db         69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88

Qy       1350 AAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAA 1409
Db         89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108

Qy       1410 GAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGAC 1469
Db        109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128

Qy       1470 CATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGAT 1529
Db        129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148

Qy       1530 GCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
Db        149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVa 168

Qy       1590 GCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAATTAATCTCAA 1649
Db        168 lLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188

Qy       1650 TTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCACAAAGAGACC 1709
Db        188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208

Qy       1710 AACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGATN 1769
Db        208 lnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228

Qy       1770 ATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAA 1829
Db        228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248

Qy       1830 GCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGACAACAAA 1889
Db        248 erLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267

Qy       1890 AGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAAA 1948
Db        268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHisLeuLeuLys 287

Qy       1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTATATTTCAATA 2008
Db        288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307

Qy       2009 TGGAAAAAAAAAAANAAAAA 2027
Db        307 rGluLysGluLysAlaGlu 313

RESULT 34
US-09-834-759-483
; Sequence 483, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C9
;  CURRENT APPLICATION NUMBER: US/09/834,759
;  CURRENT FILING DATE:  2001-04-13
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 483
;   LENGTH: 323
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-759-483

Alignment Scores:
Pred. No.:              5.41e-124       Length:         323
Score:                  1397.00         Matches:        288
Percent Similarity:     94.50%          Conservative:   4
Best Local Similarity:  93.20%          Mismatches:     13
Query Match:            41.05%          Indels:         5
DB:                     4               Gaps:           0

US-09-602-362E-15 (1-2030) x US-09-834-759-483 (1-323)

Qy       1110 CAGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGTTGAAA 1169
Db          9 GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys 28

Qy       1170 AAGGAAATTGCCATGCTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAAG 1229
Db         29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48

Qy       1230 GAAAATAAATACTTTGAGGACATTAAGATTTTAAAAGAAAAGAATGCTGAACTTCAGATG 1289
Db         49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68

Qy       1290 ACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGGGCATCTCAATATAGTGGGCAGCTT 1349
Db         69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88

Qy       1350 AAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAAATTGAAGGAAAAACAAGACAAA 1409
Db         89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108

Qy       1410 GAAATACTAGAGGCAGAAATTGAATCACACCATCCTAGACTGGCTTCTGCTGTACAAGAC 1469
Db        109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128

Qy       1470 CATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGAT 1529
Db        129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148

Qy       1530 GCTTGTTTGCAAAGAAAAATGAATGTTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
Db        149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVa 168

Qy       1590 GCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCANAAGCCTAAAAATTAATCTCAA 1649
Db        168 lLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188

Qy       1650 TTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGGAACATGCACAAAGAGACC 1709
Db        188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208

Qy       1710 AACGTGAAACACAGTGTCAAATGAAGGAAGCTGAACACATGTNTCAAANCGAACAAGATN 1769
Db        208 lnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228

Qy       1770 ATGTGAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAA 1829
Db        228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248

Qy       1830 GCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGACAACAAA 1889
Db        248 erLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267

Qy       1890 AGCAAGATAACAATTGATNTTCATTNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAAA 1948
Db        268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHisLeuLeuLys 287

Qy       1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTAAAAAACCCGTATATTTCAATA 2008
Db        288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307
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